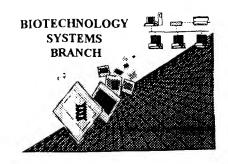
## RAW SEQUENCE LISTING ERROR REPORT



#5

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/83/.95/Source: 9/5/200/

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

## PCT09

DATE: 09/05/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/831,951 TIME: 13:21:11 Input Set : A:\Osanai Seq Lst 8-14-01.txt Output Set: N:\CRF3\09052001\I831951.raw Does Not Comply Corrected Diskette Needled 1 <110 > APPLICANT: Osanai, Tomohiro 2 Magota, Köji W--> 3 <120> TITLE OF INVENTION: Inhibitor and Activator of Coupling Factor-6 and Antigen thereto W--> 4 <130> FILE REFERENCE: 46220 -M1-2 W--> 5 <140> CURRENT APPLICATION NUMBER: US 09/831,951 6 <141 · CURRENT FILING DATE: 2001-05-16 J <150 - PRIOR APPLICATION NUMBER: JPA 264687/99 3 <151 - PRIOR FILING DATE: 1999-39-17 9 <160> NUMBER OF SEQ ID: 24 ERRORED SEQUENCES 117 <210 - SEP ID NO: 6 118 <311 · LENGTH: 23 119 KG12 - TYFE: DNA 120 K213 - OBGANISM: Artificial Sequence W--> 121 <220> FEATURE: W--> 122 <221> NAME/KEY: 123 K2220 LOCATION: 124 KODEN OTHER INFORMATION: Primer used in PCR method 236 uset amulatur base Lotal at right margin of soul line W--> 125 <400> SEQUENCE: 6 E--> 126 atgactgttc agaggatctt cag 129 KUION SECTE NO: 130 GIII: LENGTE: 27 131 REIDE TYPE: DNA 131 H213 OF GANISM: Artificial Sequence W--> 133 <220> FEATURE: W--> 134 <221> NAME/KEY: 135 HIZZE LOCATION: 136 - 223 - OTHER INFORMATION: Primer used in PCR method W--> 137 <400> SEQUENCE: 7 276-42et E--> 138 gtcgactcag gactggggtt tgtcgag 141 Filtor SBD ID NO: 8 140 - 11 LENGTH: 23 14% of Los TYPE: CNA 144 - MISS OF CANISM: Artificial Sequence W--> 145 <220> FEATURE: W--> 146 <221> NAME/KEY: 147 Challe Location:  $14 \text{ M} \cdot 0.2230 \cdot \text{OTHER}$  INFORMATION: Primer used in PCR method W--> 149 <400> SEQUENCE: 8 23 (-E--> 150 atgattcttc agaggctctt cag 153 M.1100 SEQ II NO: 9 154 (211) LENGTH: 28

196 - 21 - ORGANISM: Artificial Sequence

155 KRILE: TYPE: DNA

RAW SEQUENCE LISTING

DATE: 09/05/2001

PATENT APPLICATION: US/09/831,951

TIME: 13:21:11

Input Set: A:\Osanai Seq Lst 8-14-01.txt Output Set: N:\CRF3\09052001\I831951.raw

W--> 157 <220> FEATURE:

W--> 158 <221> NAME/KEY:

153 <222 LOCATION:

160 NAMES OTHER INFORMATION: Primer used in 10% method

W--> 161 <400> SEQUENCE: 9

E--> 162 gtcgactcag gcctggggtt tttcgatg

786-

165 <310 - SEQ ID NO: 10

166 KILL LENGTH: 45

167 HUIL - TYPE: DNA

16: CALL ORGANISM: Artificial Sequence

W--> 169 <220> FEATURE:

W--> 170 <221> NAME/KEY:

171 RUSSE BOCKTION:

177 AMPRO DIHER INFORMATION: Gene coding for enterokinase recognition site and Eco RI

recognition

1 7 % 3:te

W--> 174 <400> SEQUENCE: 10

E--> 175 gaattcgacg atgacgataa gaataaggaa cttgatcctg tacag

456-

178 \*2100 SED ID NO: 11

179 - .:111: LENGTE: 46

140 Chill TYPE: INA

181 (L199 OF MANISM: Artificial Sequence

W--> 182 <220> FEATURE:

W--> 183 <221> NAME/KEY:

184 (LUI) LOCATION:

115 First CIMER IMPORMATION: Gene coding for enterokinase recognition site and Eco RI recognition.

186

W--> 187 <400> SEQUENCE: 11

E--> 188 gaattcgacg atgacgataa gaataaggaa cttgatccta tacaga

46 6-

295 KUTO SEQ ID NO: 22

296 KLIID LENGTE: 31

297 WILL TYPE: INA

298 HL18 OFGANISM: Artificial Sequence

W--> 299 <220> FEATURE:

W--> 300 <221> NAME/KEY:

301 HILLS LOCATION:

SOL HILLS OTHER INFORMATION: Primer for ECR method

ence

for ECR method

insirt or sporce of the lock group of 10 bases

in a

non-coding

regioner W--> 303 <400> SEQUENCE: 22 /

E--> 304 gatcgagggacgtaataaggaacttgatcct

307 k. 100 SEQ 1D NO: 213 30% - 1211: LENGTH: 26

30 + HAIL TYPE: CNA

310 ALTIG OF GANIEM: Artificial Sequence

W--> 311 <220> FEATURE:

W--> 312 <221> NAME/KEY:

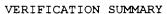
31: KULLE LOCATION: 314 KULLE OTHER INFORMATION: Primer for FCR method

W--> 315 <400> SEQUENCE: 23

E--> 316 gtcgacttaggactggggtttgtcga

26

separate into groupe of 10

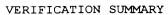


PATENT APPLICATION: US/09/831,951

TATE: 444 . 421 TIME: 14:21:12

Imput Set : A:\Osanai Seq Lst 8-14-01.txt
Output Set: N:\CRF3\09052001\I831951.raw

```
L:3 M:28? W: Missing Blank Line separator, - 120 - field identifier
L:: M: M8 · W: Missing Blank Line separator, · 130 · field identifier
L:5 M:ME - W: Missing Blank Line separator, +144 - field identifier
L: / M:::8 · W: Missing Plank Line separator, · le · field identifier
L:16 M:2:3 W: M:ssing Blank Line separator, +400 - figli identifier
L:3 . M:2%3 W: Missing Blank Line separator, .400 . field identifier
L:6. M:283 W: Missing Blank Line separator, +220 - field identitier
L:6: M:257 W: Festure value mis-spelled or invalid, +221: Name/Key for NEQ ID#:3
L:0 M:2-3 W: Missing Blank Line separator, +400 - field identifier
L: '4 M:2-3 W: M.ssing Blank Line separator, \pm 400 \pm {\rm field} identifier
L:1:0 M:.83 W: Missing blank Line separator, 400> field identifier
L:1.1 M:183 W: Missing Blank Line separator, 2202 field identifier
L:1.1 M:187 W: Feature value mis-spelled in invalid, 2212 Name Key for FEQ ID#:6
L:1.5 H:183 W: Missing Flank Line separator, 400> field identifier
L:1.6 M:154 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:6
L:100 M:133 W: Missing Blank Line separator, 2200 field identifier
L:1-4 M:187 W: Feature value mis-spelled or invalid, - 201> Name Key for SEQ ID#:7
L:l: M:185 W: Missing Blank Line separator, 400% field identifier
L:1.8 M:154 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:7
L:14% M:18% W: Missing Flank Line separator, 220% field identifier
L:146 M:257 W: Feature value mis-spelled in invalid, -221> Name Key for SEQ ID#:8
L:14: M:3:3 W: Missing Blank Line separator, <4000 field identifier
L:19: M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:8
L:15 M:283 W: Missing Flank Line separator, <220> field identifier
L:46 - M:057 W: Feature value mis-spelled or invalid, -221> Name Yey for SEQ ID#:9
L:1-1 M:18: W: Missing Blank Line separator, *400> field identifier
L:led M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:9
L:109 M:283 W: Missing Blank Line separator, <220> field identifie:
L:17 M:257 W: Feature value mis-spelled or invalid, <221> Name Key for SEQ ID#:10
L:1'4 M:Lii W: Missing Blank Line separator, 400> field identifier
L:175 M:254 E: No. of Bases conflict, LENGTH:Imput:0 Gounted:45 SEQ:10
L:18. M:183 W: Missing Blank Line separator, 3220> field identifier
L:18: M:157 W: Feature value mis-spelled or invalid, +221 / Name/Key for SEQ ID#:11
L:187 M:183 W: Missing Blank Line separator, 450/ field identifier
L:184 M:184 E: No. of Bases conflict, LENGTH:Input:0 Counted:46 SEQ:11
L:196 M:183 W: Missing Blank Line separator, <400% field identifier
L:D00 M:183 W: Missing Blank Line separator, <400> field identifier
L:100 M:263 W: Missing Blank Line separator, 400 field identifier L:107 M:263 W: Missing Blank Line separator, 400 field identifier L:107 M:263 W: Missing Blank Line separator, 400 field identifier L:100 M:263 W: Missing Blank Line separator, 400 field identifier
L:Les M:L83 W: Missing Blank Line separator, *400x field identified
L:Der M:183 W: Missing Blank Line separator, 4000 field identifier
L:27- M:183 W: Missing Blank Line Séparator, 4000 field identifies
L:De7 M:DE3 W: Missing Blank Line separator, <220 field identifier
L:200 M:057 W: Feature value mis-spelled or invalid, 02210 Name Key for SEQ ID#:21
L:231 M:183 W: Missing Blank Line separator, 4000 field identifier
1:29. M:283 W: Missing Blank Line separator, - 220. field identifier
```



PATENT APPLICATION: US/09/831,951

1,ATE: \*\*\*\*... | 1 TIME: 1::21:1...

Input Set : A:\Osanai Seq Lst 8-14-01.txt
Output Set: N:\CRF3\09052001\1831951.raw

L:300 M:257 W:	Feature value mis-spelled or invalit, +221 - Name/Key for JEQ 10#:22
L:303 M:283 W:	Missing Blank Line separator, 44 field identifier
L:304 M:254 E:	No. of Bases conflict, LENGTH:Input:@ Counted:31 SEQ:22
	Missing Plank Line separator, A. Teld identifier
	Feature value mis-spelled r invalid, +221 + Name/Key for fBL 10#:23
	Missing Blank Line separator, +4 * + tield in-ntitier
	No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:23
	Missing Blank Line separator, <220 field identifier
	Feature value mis-spelled or invalid, <221 · Name/Key for SEQ ID#:24
L:327 M:283 W:	Missing Blank Line separator, +40% - field identifie: